Metabolic, Replication and Genomic Category of Systems in Biology, Bioinformatics and Medicine

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1. Introduction : Abstract Metabolic-Replication Systems

Robert Rosen introduced metabolic-repair models, or (**M,R**)-systems in mathematical biology (abstract relational biology) in 1957 ([4,5]); such systems will be here abbreviated as MR-systems, (or simply MR's). Rosen, then represented the MR's in terms of categories of sets, deliberately selected without any structure other than the *discrete topology of sets*.

Theoreticians of life's origins postulate that Life on Earth has begun with the simplest possible organism, called the primordial. Mathematicians interested in biology and this important question of the minimal living organism have attempted to define the functional relations that would have made life possible in such a minimal system- a grandad and granma of all living organisms on Earth.

Definition 1.1 The simplest MR-system is a relational model of the primordial organism which is defined by the following categorical sequence (or diagram) of sets and set-theoretical mappings: $f : A \to B, \phi : B \to Hom_{MR}(A, B)$, where A is the set of inputs

to the MR-system, B is the set of its outputs, and ϕ is the `repair map', or $R$-component, of the $MR$-system which associates to a certain product, or output $b$, the `metabolic' component (such as an enzyme, E, for example) represented by the set-theoretical mapping f. Then, $Hom_{MR}(A,B)$ is defined as the set of all such metabolic (set-theoretical) mappings (occasionally written incorrectly by some authors as $\{f\}$).

Definition 1.2 A general (M,R)-system was defined by Rosen (1958a,b) as the network or graph of the metabolic and repair components that were specified above inDefinition 0.1; such components are networked in a complex, abstract `organism' defined by all the abstract relations and connecting maps between the sets specifying all the metabolic and repair components of such a general, abstract model of the biological organism. The mappings bettwen (M,R)-systems are defined as the the metabolic and repair set-theoretical mappings, such as f and ϕ (specified inDefinition 0.1); moreover, there is also a finite number of sets (just like those that are defined as in Definition 0.1): A_i, B_i, whereas $f \in Hom_{MR_i}(A_i,B_i)$ and $\phi \in Hom_{MR_i}[B, Hom_{MR_i}(A_i,B_i)]$, with $i \in I$, and I being a finite index set, or directed set, with (f,ϕ) being a finite number of distinct metabolic and repair components pairs. Alternatively, one may think of a a general MR-system as being `made of' a finite number N of interconnected MR_i, metabolic-repair modules with input sets A_i and output sets B_i. To sum up: a general MR-system can be defined as a family of interconnected quartets: $\{(A_i, B_i, f_i, \phi_i)\}_{i \in I}$, where I is an index set of integers

$i = 1, 2, ..., n$

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2. Category of (**M,R**)-Systems

Definition 1.3

A category of (M,R)-system quartet modules, $\{(A_i, B_i, f_i, \phi_i)\}_{i\in I}$, with I being an index set of integers $i = 1, 2, ..., n$, is a small category of sets with set-theoretical mappings defined by the MR-morphisms between the quarted modules $\{(A_i, B_i, f_i, \phi_i)\}_{i\in I}$, and also with repair components $\phi_i \in Hom_{MR_i}[B, Hom_{MR_i}(A_i, B_i)]$ defined as (M,R), with the -morphism composition defined by the usual composition of functions between sets.

With a few, additional notational changes it can be shown that the category of (M,R)-systems is a subcategory of the category of automata (or sequential machines), $\mathcal{S}_{[M,A]}$ ([7,8]).

Remark 1.1 For over two decades, Robert Rosen developed with several coworkers the MR-systems theory and its applications to life sciences, medicine and general systems theory. He also considered biocomplexity to be an `emergent', defining feature of organisms which is not reducible in terms of the molecular structures (or molecular components) of the organism and their physicochemical interactions. However, in his last written book in 1997 on ``Essays on Life Itself'', published posthumously in 2000, Robert Rosen finally accepted the need for representing organisms in terms of *categories with structure* that entail biological functions, both metabolic and repair ones. Note also that, unlike Rashevsky in his theory of organismic sets, Rosen did not attempt to extend the MRs to modeling societies, even though with appropriate modifications of generalized (M,R)-system categories with structure ([7,8,13]), this is feasible and yields meaningful mathematical and sociological results. Thus, subsequent publications have generalized MR-system (GMRs) and have studied the fundamental, mathematical properties of algebraic categories of GMRs that were constructed functorially based on the Yoneda-Grothendieck Lemma and construction. Then it was shown that such algebraic categories of GMRs are Cartesian closed [7]. Several molecular biology realizations of GMRs in terms of DNA, RNAs,

enzymes, $RNA \rightarrow DNA$-reverse trancriptases, and other biomolecular components were subsequently introduced and discussed in ref. [21,13,14] in terms of non-linear genetic network models in many-valued, LM_n logic algebras (or algebraic category $\mathcal{LM}$ of LM_n logic algebras).

If simple (M, R)-systems are considered as sequential machines or automata the category of (M, R)-systems and (M, R)-system homomorphisms is a subcategory of the automata category. However, when (M, R)-systems are considered together with their dynamic representations the category of dynamic (M, R)-systems is no longer a subcategory of the category of automata.

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